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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2007; month=11; day=29; hr=9; min=2; sec=32; ms=638;]

=====

Reviewer Comments:

<210> 45

<211> 6

<212> PRT

<213> Consensus

<220>

<221> misc_feature

<222> (2)..(2)

<223> 1 or i

<220>

<221> misc_feature

<222> (4)..(4)

<223> Xaa can be any naturally occurring amino acid

<400> 45

His Leu Lys Xaa Val Tyr

1 5

The above <213> response is invalid: per Sequence Rules, the only valid responses are: the Genus species of the organism, "Artificial Sequence," or "Unknown." "Artificial Sequence" and "Unknown" require explanation in the <220>-<223> section. For example, "Consensus" would be an insufficient explanation; please try to give information regarding the source or function of the genetic material. Same error in subsequent sequences.

<210> 46

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<211> 7
<212> PRT
<213> Consensus

<220>
<221> misc_feature
<222> (2)..(2)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (5)..(5)
<223> y or f

<220>
<221> misc_feature
<222> (6)..(6)
<223> Xaa can be any naturally occurring amino acid

<400> 46
Ala Xaa Gly Ala Tyr Xaa His
1                5

```

Besides an invalid <213> response, the above <223> explanation regarding the residue at location 5 is incorrect. "Tyr" is at location 5 and can only represent itself, not Phenylalanine; use "Xaa," instead, and explain in the <223> response that it can represent y or f. Same type of error in subsequent sequences.

Application No: 10548748 Version No: 2.0

Input Set:

Output Set:

Started: 2007-11-07 18:49:00.167
 Finished: 2007-11-07 18:49:06.589
 Elapsed: 0 hr(s) 0 min(s) 6 sec(s) 422 ms
 Total Warnings: 23
 Total Errors: 11
 No. of SeqIDs Defined: 69
 Actual SeqID Count: 69

Error code	Error Description
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W 402	Undefined organism found in <213> in SEQ ID (49)
W 402	Undefined organism found in <213> in SEQ ID (50)
W 402	Undefined organism found in <213> in SEQ ID (51)
W 402	Undefined organism found in <213> in SEQ ID (52)
W 402	Undefined organism found in <213> in SEQ ID (53)
W 402	Undefined organism found in <213> in SEQ ID (54)
W 402	Undefined organism found in <213> in SEQ ID (55)

Input Set:

Output Set:

Started: 2007-11-07 18:49:00.167
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Elapsed: 0 hr(s) 0 min(s) 6 sec(s) 422 ms
Total Warnings: 23
Total Errors: 11
No. of SeqIDs Defined: 69
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Error code	Error Description
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SEQUENCE LISTING

<110> Frank, Markus
Kogel, Karl-Heinz
Hueckelhoven, Ralph

<120> METHOD FOR INCREASING RESISTANCE AGAINST STRESS FACTORS IN PLANTS

<130> 12810-00137-US

<140> 10548748

<141> 2005-09-08

<150> PCT/EP2004/002436

<151> 2004-03-10

<150> DE 103 11 118.2

<151> 2003-03-12

<160> 69

<170> PatentIn version 3.4

<210> 1

<211> 744

<212> DNA

<213> Hordeum vulgare

<220>

<221> CDS

<222> (1)..(741)

<223> coding for BII-protein

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1				5					10					15		

cac	gac	tcc	ctc	aag	aac	ttc	cgc	cag	atc	tcc	ccc	gcc	gtg	cag	tcc	96
His	Asp	Ser	Leu	Lys	Asn	Phe	Arg	Gln	Ile	Ser	Pro	Ala	Val	Gln	Ser	
			20					25					30			

cac	ctc	aag	ctc	gtt	tac	ctg	act	cta	tgc	ttt	gca	ctg	gcc	tca	tct	144
His	Leu	Lys	Leu	Val	Tyr	Leu	Thr	Leu	Cys	Phe	Ala	Leu	Ala	Ser	Ser	
			35					40					45			

gcc	gtg	ggg	gct	tac	cta	cac	att	gcc	ctg	aac	atc	ggc	ggg	atg	ctg	192
Ala	Val	Gly	Ala	Tyr	Leu	His	Ile	Ala	Leu	Asn	Ile	Gly	Gly	Met	Leu	
			50				55						60			

aca	atg	ctc	gct	tgt	gtc	gga	act	atc	gcc	tgg	atg	ttc	tcg	gtg	cca	240
Thr	Met	Leu	Ala	Cys	Val	Gly	Thr	Ile	Ala	Trp	Met	Phe	Ser	Val	Pro	
			65				70					75			80	

gtc	tat	gag	gag	agg	aag	agg	ttt	ggg	ctg	ctg	atg	ggg	gca	gcc	ctc	288
Val	Tyr	Glu	Glu	Arg	Lys	Arg	Phe	Gly	Leu	Leu	Met	Gly	Ala	Ala	Leu	

85	90	95	
ctg gaa ggg gct tcg gtt gga cct	ctg att gag ctt gcc ata gac ttt	336	
Leu Glu Gly Ala Ser Val Gly Pro	Leu Ile Glu Leu Ala Ile Asp Phe		
100	105 110		
gac cca agc atc ctc gtg aca ggg ttt	gtc gga acc gcc atc gcc ttt	384	
Asp Pro Ser Ile Leu Val Thr Gly Phe	Val Gly Thr Ala Ile Ala Phe		
115	120 125		
ggg tgc ttc tct ggc gcc gcc atc atc	gcc aag cgc agg gag tac ctg	432	
Gly Cys Phe Ser Gly Ala Ala Ile Ile	Ala Lys Arg Arg Glu Tyr Leu		
130	135 140		
tac ctc ggt ggc ctg ctc tcg tct ggc	ctg tcg atc ctg ctc tgg ctg	480	
Tyr Leu Gly Gly Leu Leu Ser Ser Gly	Leu Ser Ile Leu Leu Trp Leu		
145	150 155 160		
cag ttt gtc acg tcc atc ttt ggc cac	tcc tct ggc agc ttc atg ttt	528	
Gln Phe Val Thr Ser Ile Phe Gly His	Ser Ser Gly Ser Phe Met Phe		
165	170 175		
gag gtt tac ttt ggc ctg ttg atc ttc	ctg ggg tac atg gtg tac gac	576	
Glu Val Tyr Phe Gly Leu Leu Ile Phe	Leu Gly Tyr Met Val Tyr Asp		
180	185 190		
acg cag gag atc atc gag agg gcg cac	cat ggc gac atg gac tac atc	624	
Thr Gln Glu Ile Ile Glu Arg Ala His	His Gly Asp Met Asp Tyr Ile		
195	200 205		
aag cac gcc ctc acc ctc ttc acc gac	ttt gtt gcc gtc ctc gtc cga	672	
Lys His Ala Leu Thr Leu Phe Thr Asp	Phe Val Ala Val Leu Val Arg		
210	215 220		
gtc ctc atc atc atg ctc aag aac gca	ggc gac aag tcg gag gac aag	720	
Val Leu Ile Ile Met Leu Lys Asn Ala	Gly Asp Lys Ser Glu Asp Lys		
225	230 235 240		
aag aag agg aag agg ggg tcc tga		744	
Lys Lys Arg Lys Arg Gly Ser			
245			

<210> 2

<211> 247

<212> PRT

<213> Hordeum vulgare

<400> 2

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His Asp Ser Leu Lys Asn Phe Arg Gln	Ile Ser Pro Ala Val Gln Ser
20	25 30

His Leu Lys Leu Val Tyr Leu Thr	Leu Cys Phe Ala Leu Ala Ser Ser
35	40 45

Ala Val Gly Ala Tyr Leu His Ile Ala Leu Asn Ile Gly Gly Met Leu
50 55 60

Thr Met Leu Ala Cys Val Gly Thr Ile Ala Trp Met Phe Ser Val Pro
65 70 75 80

Val Tyr Glu Glu Arg Lys Arg Phe Gly Leu Leu Met Gly Ala Ala Leu
85 90 95

Leu Glu Gly Ala Ser Val Gly Pro Leu Ile Glu Leu Ala Ile Asp Phe
100 105 110

Asp Pro Ser Ile Leu Val Thr Gly Phe Val Gly Thr Ala Ile Ala Phe
115 120 125

Gly Cys Phe Ser Gly Ala Ala Ile Ile Ala Lys Arg Arg Glu Tyr Leu
130 135 140

Tyr Leu Gly Gly Leu Leu Ser Ser Gly Leu Ser Ile Leu Leu Trp Leu
145 150 155 160

Gln Phe Val Thr Ser Ile Phe Gly His Ser Ser Gly Ser Phe Met Phe
165 170 175

Glu Val Tyr Phe Gly Leu Leu Ile Phe Leu Gly Tyr Met Val Tyr Asp
180 185 190

Thr Gln Glu Ile Ile Glu Arg Ala His His Gly Asp Met Asp Tyr Ile
195 200 205

Lys His Ala Leu Thr Leu Phe Thr Asp Phe Val Ala Val Leu Val Arg
210 215 220

Val Leu Ile Ile Met Leu Lys Asn Ala Gly Asp Lys Ser Glu Asp Lys
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Lys Lys Arg Lys Arg Gly Ser
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<212> DNA

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<221> CDS

<222> (1)..(741)

<223> coding for BI1-protein

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tgg agc tat gat tct ctt aaa aac ttc cgt cag att tct cca gcc gtt 96

Trp	Ser	Tyr	Asp	Ser	Leu	Lys	Asn	Phe	Arg	Gln	Ile	Ser	Pro	Ala	Val	
			20					25					30			
cag	aat	cat	ctt	aaa	cgg	gtt	tat	ttg	acc	tta	tgt	tgt	gct	ctt	gtg	144
Gln	Asn	His	Leu	Lys	Arg	Val	Tyr	Leu	Thr	Leu	Cys	Cys	Ala	Leu	Val	
		35					40					45				
gcg	tct	gcc	ttt	gga	gct	tac	ctc	cat	gtg	ctc	tgg	aat	atc	ggc	ggc	192
Ala	Ser	Ala	Phe	Gly	Ala	Tyr	Leu	His	Val	Leu	Trp	Asn	Ile	Gly	Gly	
	50					55					60					
att	ctt	aca	acg	att	gga	tgt	att	gga	act	atg	att	tgg	ctc	ctt	tca	240
Ile	Leu	Thr	Thr	Ile	Gly	Cys	Ile	Gly	Thr	Met	Ile	Trp	Leu	Leu	Ser	
65					70					75					80	
tgt	cct	cct	tat	gaa	cac	caa	aaa	agg	ctt	tct	ctt	ctg	ttt	gtg	tct	288
Cys	Pro	Pro	Tyr	Glu	His	Gln	Lys	Arg	Leu	Ser	Leu	Leu	Phe	Val	Ser	
				85				90						95		
gct	gtt	ctt	gaa	ggc	gct	tct	gtt	ggc	ccc	ttg	atc	aaa	gtg	gca	att	336
Ala	Val	Leu	Glu	Gly	Ala	Ser	Val	Gly	Pro	Leu	Ile	Lys	Val	Ala	Ile	
			100					105					110			
gat	gtt	gac	cca	agc	atc	ctt	atc	act	gca	ttt	gtt	gga	act	gcg	ata	384
Asp	Val	Asp	Pro	Ser	Ile	Leu	Ile	Thr	Ala	Phe	Val	Gly	Thr	Ala	Ile	
		115					120					125				
gcg	ttt	gtc	tgt	ttc	tca	gca	gca	gca	atg	tta	gca	aga	cgc	agg	gag	432
Ala	Phe	Val	Cys	Phe	Ser	Ala	Ala	Ala	Met	Leu	Ala	Arg	Arg	Arg	Glu	
	130					135					140					
tat	ctc	tac	ctt	gga	gga	ctg	ctt	tca	tct	ggc	ttg	tct	atg	cta	atg	480
Tyr	Leu	Tyr	Leu	Gly	Gly	Leu	Leu	Ser	Ser	Gly	Leu	Ser	Met	Leu	Met	
145					150					155					160	
tgg	ctc	cag	ttt	gcc	tct	tca	atc	ttt	ggc	ggc	tct	gca	tct	atc	ttt	528
Trp	Leu	Gln	Phe	Ala	Ser	Ser	Ile	Phe	Gly	Gly	Ser	Ala	Ser	Ile	Phe	
				165					170					175		
aag	ttt	gag	ttg	tac	ttt	gga	ctt	ttg	atc	ttt	gtg	gga	tac	atg	gtg	576
Lys	Phe	Glu	Leu	Tyr	Phe	Gly	Leu	Leu	Ile	Phe	Val	Gly	Tyr	Met	Val	
			180					185					190			
gtg	gac	aca	caa	gag	att	ata	gaa	aag	gca	cac	ctc	ggc	gac	atg	gac	624
Val	Asp	Thr	Gln	Glu	Ile	Ile	Glu	Lys	Ala	His	Leu	Gly	Asp	Met	Asp	
		195					200					205				
tat	gta	aaa	cat	tcg	ttg	acc	ctt	ttc	act	gac	ttt	gta	gct	gtg	ttt	672
Tyr	Val	Lys	His	Ser	Leu	Thr	Leu	Phe	Thr	Asp	Phe	Val	Ala	Val	Phe	
	210					215					220					
gtt	cgg	att	ctc	atc	ata	atg	ttg	aag	aac	tca	gca	gat	aaa	gaa	gag	720
Val	Arg	Ile	Leu	Ile	Ile	Met	Leu	Lys	Asn	Ser						

gggtgttatc gtgtgtggcc actttgaaga tattacttgt tagcactctc tattggtgac 831
 cagacatggt tccactaaaa aggatctgct tgtttcactt ctgcacaagt accatcttca 891
 gattgtaaat gactcgagtg ttgtttcttct tttcataaac ttttgttctt taagagtttg 951
 gttctactga ttgcatctta ccaagctaag aataatgtag gaaaatgata atcctgttta 1011
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<211> 247

<212> PRT

<213> Arabidopsis thaliana

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Gln Asn His Leu Lys Arg Val Tyr Leu Thr Leu Cys Cys Ala Leu Val
 35 40 45

Ala Ser Ala Phe Gly Ala Tyr Leu His Val Leu Trp Asn Ile Gly Gly
 50 55 60

Ile Leu Thr Thr Ile Gly Cys Ile Gly Thr Met Ile Trp Leu Leu Ser
 65 70 75 80

Cys Pro Pro Tyr Glu His Gln Lys Arg Leu Ser Leu Leu Phe Val Ser
 85 90 95

Ala Val Leu Glu Gly Ala Ser Val Gly Pro Leu Ile Lys Val Ala Ile
 100 105 110

Asp Val Asp Pro Ser Ile Leu Ile Thr Ala Phe Val Gly Thr Ala Ile
 115 120 125

Ala Phe Val Cys Phe Ser Ala Ala Ala Met Leu Ala Arg Arg Arg Glu
 130 135 140

Tyr Leu Tyr Leu Gly Gly Leu Leu Ser Ser Gly Leu Ser Met Leu Met
 145 150 155 160

Trp Leu Gln Phe Ala Ser Ser Ile Phe Gly Gly Ser Ala Ser Ile Phe
 165 170 175

Lys Phe Glu Leu Tyr Phe Gly Leu Leu Ile Phe Val Gly Tyr Met Val
 180 185 190

Val Asp Thr Gln Glu Ile Ile Glu Lys Ala His Leu Gly Asp Met Asp
 195 200 205

Tyr Val Lys His Ser Leu Thr Leu Phe Thr Asp Phe Val Ala Val Phe
 210 215 220

Val Arg Ile Leu Ile Ile Met Leu Lys Asn Ser Ala Asp Lys Glu Glu
 225 230 235 240

Lys Lys Lys Lys Arg Arg Asn
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<210> 5

<211> 1160

<212> DNA

<213> Nicotiana tabacum

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<221> CDS

<222> (1)..(747)

<223> coding for BII-protein

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aat cgc tgg agt tac gat tct ctt aag aac ttc cgc cag atc tct ccc 96
 Asn Arg Trp Ser Tyr Asp Ser Leu Lys Asn Phe Arg Gln Ile Ser Pro
 20 25 30

ttt gtt caa act cat ctc aaa aag gtc tac ctt tca tta tgt tgt gct 144
 Phe Val Gln Thr His Leu Lys Lys Val Tyr Leu Ser Leu Cys Cys Ala
 35 40 45

tta gtt gct tcg gct gct gga gct tac ctt cac att ctt tgg aac att 192
 Leu Val Ala Ser Ala Ala Gly Ala Tyr Leu His Ile Leu Trp Asn Ile
 50 55 60

ggg ggc tta ctt acg aca ttg gga tgt gtg gga agc ata gtg tgg ctg 240
 Gly Gly Leu Leu Thr Thr Leu Gly Cys Val Gly Ser Ile Val Trp Leu
 65 70 75 80

atg gcg aca cct ctg tat gaa gag caa aag agg ata gca ctt ctg atg 288
 Met Ala Thr Pro Leu Tyr Glu Glu Gln Lys Arg Ile Ala Leu Leu Met
 85 90 95

gca gct gca ctg ttt aaa gga gca tct att ggt cca ctg att gaa ttg 336
 Ala Ala Ala Leu Phe Lys Gly Ala Ser Ile Gly Pro Leu Ile Glu Leu
 100 105 110

gct att gac ttt gac cca agc att gtg atc ggt gct ttt gtt ggt tgt 384
 Ala Ile Asp Phe Asp Pro Ser Ile Val Ile Gly Ala Phe Val Gly Cys
 115 120 125

gct gtg gct ttt ggt tgc ttc tca gct gct gcc atg gtg gca agg cgc 432
 Ala Val Ala Phe Gly Cys Phe Ser Ala Ala Ala Met Val Ala Arg Arg
 130 135 140

aga gag tac ttg tat ctt gga ggt ctt ctt tca tct ggt ctc tct atc 480
 Arg Glu Tyr Leu Tyr Leu Gly Gly Leu Leu Ser Ser Gly Leu Ser Ile
 145 150 155 160

ctt ttc tgg ttg cac ttc gcg tcc tcc att ttt ggt ggt tct atg gcc 528
 Leu Phe Trp Leu His Phe Ala Ser Ser Ile Phe Gly Gly Ser Met Ala
 165 170 175

ttg ttc aag ttc gag gtt tat ttt ggg ctc ttg gtg ttt gtg ggc tat 576
 Leu Phe Lys Phe Glu Val Tyr Phe Gly Leu Leu Val Phe Val Gly Tyr
 180 185 190

atc att ttt gac acc caa gat ata att gag aag gca cac ctt ggg gat 624
 Ile Ile Phe Asp Thr Gln Asp Ile Ile Glu Lys Ala His Leu Gly Asp
 195 200 205

ttg gac tac gtg aag cat gct ctg acc ctc ttt aca gat ttt gtt gct 672
 Leu Asp Tyr Val Lys His Ala Leu Thr Leu Phe Thr Asp Phe Val Ala
 210 215 220

gtt ttt gtg cga ata tta atc ata atg ctg aag aat gca tcc gac aag 720
 Val Phe Val Arg Ile Leu Ile Ile Met Leu Lys Asn Ala Ser Asp Lys
 225 230 235 240

gaa gag aag aag aag aag agg aga aac taatgcataa gcggttatcc 767
 Glu Glu Lys Lys Lys Lys Arg Arg Asn
 245

aaagactctg taactctaga atctggcatt ttcttggttca taaacttctg tagaccttcg 827

acaagtatgt tgttaatagt ttggtaacgc ctcagattaa gctgcgaggc tctgttatgc 887

cgcattgccaa tgtggttatg gtggtacata gatgggtttg tttccgaagc ataccatcaa 947

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<212> PRT

<213> Nicotiana tabacum

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 20 25 30

Phe Val Gln Thr His Leu Lys Lys Val Tyr Leu Ser Leu Cys Cys Ala

35

40

45

Leu Val Ala Ser Ala Ala Gly Ala Tyr Leu His Ile Leu Trp Asn Ile
50 55 60

Gly Gly Leu Leu Thr Thr Leu Gly Cys Val Gly Ser Ile Val Trp Leu
65 70 75 80

Met Ala Thr Pro Leu Tyr Glu Glu Gln Lys Arg Ile Ala Leu Leu Met
85 90 95

Ala Ala Ala Leu Phe Lys Gly Ala Ser Ile Gly Pro Leu Ile Glu Leu
100 105 110

Ala Ile Asp Phe Asp Pro Ser Ile Val Ile Gly Ala Phe Val Gly Cys
115 120 125

Ala Val Ala Phe Gly Cys Phe Ser Ala Ala Ala Met Val Ala Arg Arg
130 135 140

Arg Glu Tyr Leu Tyr Leu Gly Gly Leu Leu Ser Ser Gly Leu Ser Ile
145 150 155 160

Leu Phe Trp Leu His Phe Ala Ser Ser Ile Phe Gly Gly Ser Met Ala
165 170 175

Leu Phe Lys Phe Glu Val Tyr Phe Gly Leu Leu Val Phe Val Gly Tyr
180 185 190

Ile Ile Phe Asp Thr Gln Asp Ile Ile Glu Lys Ala His Leu Gly Asp
195